OIPE

RAW SEQUENCE LISTING DATE: 03/12/2002
PATENT APPLICATION: US/09/873,829 TIME: 09:54:51

Input Set : N:\Crf3\RULE60\09873829.raw
Output Set: N:\CRF3\03122002\I873829.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Choi, Yongwon
Wong, Brian
Josien, Regis
Steinman, Ralph

(ii) TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE THEREOF

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Klauber & Jackson
(B) STREET: 411 Hackensack Avenue, 4th Floor
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
C--> **(A) APPLICATION NUMBER: US/09/873,829**
C--> **(B) FILING DATE: 04-Jun-2001**
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 09/210,115
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-200 CIP N

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 201-487-5800
(B) TELEFAX: 201-343-1684
(C) TELEX: 133521

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1823 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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```
     (ii) MOLECULE TYPE: cDNA
    (iii) HYPOTHETICAL: NO
     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo sapiens
     (ix) FEATURE:
          (A) NAME/KEY: CDS
          (B) LOCATION: 1..738
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
CAG ATG GAT CCT AAT AGA ATA TCA GAA GAT GGC ACT CAC TGC ATT TAT        48
Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
 1               5                  10                  15
AGA ATT TTG AGA CTC CAT GAA AAT GCA GAT TTT CAA GAC ACA ACT CTG        96
Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
            20                  25                  30
GAG AGT CAA GAT ACA AAA TTA ATA CCT GAT TCA TGT AGG AGA ATT AAA       144
Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
        35                  40                  45
CAG GCC TTT CAA GGA GCT GTG CAA AAG GAA TTA CAA CAT ATC GTT GGA       192
Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
    50                  55                  60
TCA CAG CAC ATC AGA GCA GAG AAA GCG ATG GTG GAT GGC TCA TGG TTA       240
Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
65                  70                  75                  80
GAT CTG GCC AAG AGG AGC AAG CTT GAA GCT CAG CCT TTT GCT CAT CTC       288
Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
                85                  90                  95
ACT ATT AAT GCC ACC GAC ATC CCA TCT GGT TCC CAT AAA GTG AGT CTG       336
Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
            100                 105                 110
TCC TCT TGG TAC CAT GAT CGG GGG TGG GGT AAG ATC TCC AAC ATG ACT       384
Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
        115                 120                 125
TTT AGC AAT GGA AAA CTA ATA GTT AAT CAG GAT GGC TTT TAT TAC CTG       432
Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
    130                 135                 140
TAT GCC AAC ATT TGC TTT CGA CAT CAT GAA ACT TCA GGA GAC CTA GCT       480
Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
145                 150                 155                 160
ACA GAG TAT CTT CAA CTA ATG GTG TAC GTC ACT AAA ACC AGC ATC AAA       528
Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
                165                 170                 175
ATC CCA AGT TCT CAT ACC CTG ATG AAA GGA GGA AGC ACC AAG TAT TGG       576
Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
            180                 185                 190
TCA GGG AAT TCT GAA TTC CAT TTT TAT TCC ATA AAC GTT GGT GGA TTT       624
Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
        195                 200                 205
TTT AAG TTA CGG TCT GGA GAG GAA ATC AGC ATC GAG GTC TCC AAC CCC       672
Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
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PATENT APPLICATION: US/09/873,829 TIME: 09:54:52

Input Set : N:\Crf3\RULE60\09873829.raw
Output Set: N:\CRF3\03122002\I873829.raw

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127     210                 215                 220
129 TCC TTA CTG GAT CCG GAT CAG GAT GCA ACA TAC TTT GGG GCT TTT AAA       720
130 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
131 225                 230                 235                 240
133 GTT CGA GAT ATA GAT TGA GCCCCAGTTT TTGGAGTGTT ATGTATTTCC              768
134 Val Arg Asp Ile Asp  *
135                 245
137 TGGATGTTTG GAAACATTTT TTAAAACAAG CCAAGAAAGA TGTATATAGG TGTGTGAGAC     828
139 TACTAAGAGG CATGGCCCAA CGGTACACGA CTCAGTATCC ATGCTCTTGA CCTTGTAGAG     888
141 AACACGCGTA TTTACAGCCA GTGGGAGATG TTAGACTCAT GGTGTGTTAC ACAATGGTTT     948
143 TTAAATTTTG TAATGAATTC CTAGAATTAA ACCAGATTGG AGCAATTACG GGTTGACCTT    1008
145 ATGAGAAACT GCATGTGGGC TATGGGAGGG GTTGGTCCCT GGTCATGTGC CCCTTCGCAG    1068
147 CTGAAGTGGA GAGGGTGTCA TCTAGCGCAA TTGAAGGATC ATCTGAAGGG GCAAATTCTT    1128
149 TTGAATTGTT ACATCATGCT GGAACCTGCA AAAAATACTT TTTCTAATGA GGAGAGAAAA    1188
151 TATATGTATT TTTATATAAT ATCTAAAGTT ATATTTCAGA TGTAATGTTT TCTTTGCAAA    1248
153 GTATTGTAAA TTATATTTGT GCTATAGTAT TTGATTCAAA ATATTTAAAA ATGTCTTGCT    1308
155 GTTGACATAT TTAATGTTTT AAATGTACAG ACATATTTAA CTGGTGCACT TTGTAAATTC    1368
157 CCTGGGGAAA ACTTGCAGCT AAGGAGGGGA AAAAATGTTG TTTCCTAATA TCAAATGCAG    1428
159 TATATTTCTT CGTTCTTTTT AAGTTAATAG ATTTTTTCAG ACTTGTCAAG CCTGTGCAAA    1488
161 AAAATTAAAA TGGATGCCTT GAATAATAAG CAGGATGTTG GCCACCAGGT GCCTTTCAAA    1548
163 TTTAGAAACT AATTGACTTT AGAAAGCTGA CATTGCCAAA AAGGATACAT AATGGGCCAC    1608
165 TGAAATCTGT CAAGAGTAGT TATATAATTG TTGAACAGGT GTTTTTCCAC AAGTGCCGCA    1668
167 AATTGTACCT TTTTTTGTTT TTTTCAAAAT AGAAAAGTTA TTAGTGGTTT ATCAGCAAAA    1728
169 AAGTCCAATT TTAATTTAGT AAATGTTATC TTATACTGTA CAATAAAAAC ATTGCCTTTG    1788
171 AATGTTAATT TTTTGGTACA AAAGTCGACG GCCGC                              1823
174 (2) INFORMATION FOR SEQ ID NO: 2:
176      (i) SEQUENCE CHARACTERISTICS:
177           (A) LENGTH: 245 amino acids
178           (B) TYPE: amino acid
179           (D) TOPOLOGY: linear
181      (ii) MOLECULE TYPE: protein
183      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
185 Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
186   1               5                  10                  15
188 Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
189              20                  25                  30
191 Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
192          35                  40                  45
194 Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
195      50                  55                  60
197 Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
198  65                  70                  75                  80
200 Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
201                  85                  90                  95
203 Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
204              100                 105                 110
206 Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
207          115                 120                 125
209 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
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Input Set : N:\Crf3\RULE60\09873829.raw
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```
210     130                 135                 140
212 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
213 145                 150                 155                 160
215 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
216                 165                 170                 175
218 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
219             180                 185                 190
221 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
222         195                 200                 205
224 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
225     210                 215                 220
227 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
228 225                 230                 235                 240
230 Val Arg Asp Ile Asp
231                 245
233 (2) INFORMATION FOR SEQ ID NO: 3:
235      (i) SEQUENCE CHARACTERISTICS:
236           (A) LENGTH: 2237 base pairs
237           (B) TYPE: nucleic acid
238           (C) STRANDEDNESS: double
239           (D) TOPOLOGY: linear
241     (ii) MOLECULE TYPE: cDNA
243    (iii) HYPOTHETICAL: NO
245     (vi) ORIGINAL SOURCE:
246           (A) ORGANISM: Mus musculus
248     (ix) FEATURE:
249           (A) NAME/KEY: CDS
250           (B) LOCATION: 142..1092
253     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
255 CCCACGTCCC GGGGAGCCAC TGCCAGGACC TTTGTGAACC GGTCGGGGCG GGGGCCGTGG      60
257 CGGAGTCTGC TCGGCGGTGG GTGGCCCGAG AAGGGAGAGA ACGATCGCGG AGCAGGGCGC     120
259 CCGAACTCCG GGCGCCGCGC C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG       171
260                          Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys
W--> 261                                 250                 255
263 TAC CTG CGC AGC TCG GAA GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC       219
264 Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His
W--> 265             260                 265                 270
267 GAA GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA       267
268 Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro
W--> 269         275                 280                 285
271 CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG       315
272 Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu
W--> 273     290                 295                 300
275 GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG       363
276 Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln
W--> 277 305                 310                 315                 320
279 ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA       411
280 Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg
W--> 281                 325                 330                 335
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```
     284 ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG       459
     284 Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu
W--> 285             340                 345                 350
     287 AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT       507
     288 Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe
W--> 289         355                 360                 365
     291 CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC       555
     292 Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg
W--> 293     370                 375                 380
     295 TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC       603
     296 Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala
W--> 297 385                 390                 395                 400
     299 CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT       651
     300 Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn
W--> 301                 405                 410                 415
     303 GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG       699
     304 Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp
W--> 305             420                 425                 430
     307 TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC       747
     308 Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn
W--> 309         435                 440                 445
     311 GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC       795
     312 Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn
W--> 313     450                 455                 460
     315 ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT       843
     316 Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr
W--> 317 465                 470                 475                 480
     319 CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT       891
     320 Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser
W--> 321                 485                 490                 495
     323 TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT       939
     324 Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn
W--> 325             500                 505                 510
     327 TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC       987
     328 Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu
W--> 329         515                 520                 525
     331 CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG      1035
     332 Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu
W--> 333     530                 535                 540
     335 GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC      1083
     336 Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp
W--> 337 545                 550                 555                 560
     339 ATA GAC TGA GACTCATTTC GTGGAACATT AGCATGGATG TCCTAGATGT              1132
     340 Ile Asp  *
     343 TTGGAAACTT CTTAAAAAAT GGATGATGTC TATACATGTG TAAGACTACT AAGAGACATG     1192
     345 GCCCACGGTG TATGAAACTC ACAGCCCTCT CTCTTGAGCC CTGTACAGGT TGTGTATATG     1252
     347 TAAAGTCCAT AGGTGATGTT AGATTCATGG TGATTACACA ACGGTTTTAC AATTTTGTAA     1312
     349 TGATTTCCTA GAATTGAACC AGATTGGGAG AGGTATTCCG ATGCTTATGA AAAACTTACA     1372
     351 CGTGAGCTAT GGAAGGGGGT CACAGTCTCT GGTCTAACCC CTGGACATGT GCCACTGAGA     1432
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VERIFICATION SUMMARY DATE: 03/12/2002
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Input Set : N:\Crf3\RULE60\09873829.raw
Output Set: N:\CRF3\03122002\I873829.raw

L:31 M:220 C: Keyword misspelled or invalid format. [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format. [(B) FILING DATE:]
L:261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:269 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:289 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:293 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:297 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:301 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:305 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:309 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:313 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:317 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:321 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:325 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:329 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:333 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:337 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3